



UNITED STATES PATENT AND TRADEMARK OFFICE

UNITED STATES DEPARTMENT OF COMMERCE
United States Patent and Trademark Office
Address: COMMISSIONER FOR PATENTS
P.O. Box 1450
Alexandria, Virginia 22313-1450
www.uspto.gov

APPLICATION NO.	FILING DATE	FIRST NAMED INVENTOR	ATTORNEY DOCKET NO.	CONFIRMATION NO.
10/680,349	10/07/2003	David H. Walker	D6152CIP2/D1/D	5963

7590

03/24/2005

David L. Parker
FULBRIGHT & JAWORSKI L.L.P.
600 Congress Avenue
Suite 2400
Austin, TX 78701

EXAMINER

MINNIFIELD, NITA M

ART UNIT

PAPER NUMBER

1645

DATE MAILED: 03/24/2005

Please find below and/or attached an Office communication concerning this application or proceeding.

Office Action Summary

Application No.

10/680,349

Applicant(s)

WALKER ET AL.

Examiner

N. M. Minnifield

Art Unit

1645

-- The MAILING DATE of this communication appears on the cover sheet with the correspondence address --

Period for Reply

A SHORTENED STATUTORY PERIOD FOR REPLY IS SET TO EXPIRE 3 MONTH(S) FROM THE MAILING DATE OF THIS COMMUNICATION.

- Extensions of time may be available under the provisions of 37 CFR 1.136(a). In no event, however, may a reply be timely filed after SIX (6) MONTHS from the mailing date of this communication.
- If the period for reply specified above is less than thirty (30) days, a reply within the statutory minimum of thirty (30) days will be considered timely.
- If NO period for reply is specified above, the maximum statutory period will apply and will expire SIX (6) MONTHS from the mailing date of this communication.
- Failure to reply within the set or extended period for reply will, by statute, cause the application to become ABANDONED (35 U.S.C. § 133). Any reply received by the Office later than three months after the mailing date of this communication, even if timely filed, may reduce any earned patent term adjustment. See 37 CFR 1.704(b).

Status

- 1) ☒ Responsive to communication(s) filed on 05 January 2005.
- 2a) ☐ This action is **FINAL**. 2b) ☒ This action is non-final.
- 3) ☐ Since this application is in condition for allowance except for formal matters, prosecution as to the merits is closed in accordance with the practice under *Ex parte Quayle*, 1935 C.D. 11, 453 O.G. 213.

Disposition of Claims

- 4) ☒ Claim(s) 1 and 2 is/are pending in the application.
- 4a) Of the above claim(s) _____ is/are withdrawn from consideration.
- 5) ☐ Claim(s) _____ is/are allowed.
- 6) ☒ Claim(s) 1 and 2 is/are rejected.
- 7) ☐ Claim(s) _____ is/are objected to.
- 8) ☐ Claim(s) _____ are subject to restriction and/or election requirement.

Application Papers

- 9) ☒ The specification is objected to by the Examiner.
- 10) ☒ The drawing(s) filed on 07 October 2003 is/are: a) ☒ accepted or b) ☐ objected to by the Examiner.
Applicant may not request that any objection to the drawing(s) be held in abeyance. See 37 CFR 1.85(a).
Replacement drawing sheet(s) including the correction is required if the drawing(s) is objected to. See 37 CFR 1.121(d).
- 11) ☐ The oath or declaration is objected to by the Examiner. Note the attached Office Action or form PTO-152.

Priority under 35 U.S.C. § 119

- 12) ☐ Acknowledgment is made of a claim for foreign priority under 35 U.S.C. § 119(a)-(d) or (f).
- a) ☐ All b) ☐ Some * c) ☐ None of:
1. ☐ Certified copies of the priority documents have been received.
2. ☐ Certified copies of the priority documents have been received in Application No. _____.
3. ☐ Copies of the certified copies of the priority documents have been received in this National Stage application from the International Bureau (PCT Rule 17.2(a)).

* See the attached detailed Office action for a list of the certified copies not received.

Attachment(s)

- 1) ☒ Notice of References Cited (PTO-892) 2 sheets
- 2) ☐ Notice of Draftsperson's Patent Drawing Review (PTO-948)
- 3) ☒ Information Disclosure Statement(s) (PTO-1449 or PTO/SB/08)
Paper No(s)/Mail Date 1/5/05 3 sheets

- 4) ☐ Interview Summary (PTO-413)
Paper No(s)/Mail Date. _____
- 5) ☐ Notice of Informal Patent Application (PTO-152)
- 6) ☐ Other: _____

DETAILED ACTION

1. Applicant's election of species of SEQ ID NO: 41 and 42 in the reply filed on January 5, 2005 is acknowledged. Because applicant did not distinctly and specifically point out the supposed errors in the restriction requirement, the election has been treated as an election without traverse (MPEP § 818.03(a)).
2. Applicants' amendment filed January 5, 2005 is acknowledged and has been entered. Claims 1 and 2 have been amended.
3. Claims 1 and 2 are rejected under 35 U.S.C. 112, second paragraph, as being indefinite for failing to particularly point out and distinctly claim the subject matter which applicant regards as the invention. The claims are vague and indefinite in the recitation of "an amino acid sequence". Does Applicant intend for this phrase to define the entire amino acid sequence of SEQ ID NO: 2 or a fragment of the amino acid sequence of SEQ ID NO: 2?
4. The disclosure is objected to because of the following informalities: the continuity data should be updated on page 1 of the specification. Appropriate correction is required.
5. The following is a quotation of the appropriate paragraphs of 35 U.S.C. 102 that form the basis for the rejections under this section made in this Office action:

A person shall be entitled to a patent unless –

(a) the invention was known or used by others in this country, or patented or described in a printed publication in this or a foreign country, before the invention thereof by the applicant for a patent.

(b) the invention was patented or described in a printed publication in this or a foreign country or in public use or on sale in this country, more than one year prior to the date of application for patent in the United States.

(e) the invention was described in a patent granted on an application for patent by another filed in the United States before the invention thereof by the applicant for patent, or on an international application by another who has fulfilled the requirements of paragraphs (1), (2), and (4) of section 371(c) of this title before the invention thereof by the applicant for patent.

6. The changes made to 35 U.S.C. 102(e) by the American Inventors Protection Act of 1999 (AIPA) and the Intellectual Property and High Technology Technical Amendments Act of 2002 do not apply when the reference is a U.S. patent resulting directly or indirectly from an international application filed before November 29, 2000. Therefore, the prior art date of the reference is determined under 35 U.S.C. 102(e) prior to the amendment by the AIPA (pre-AIPA 35 U.S.C. 102(e)).

7. Claims 1 and 2 are rejected under 35 U.S.C. 102(e) as being anticipated by Rikihisa et al (6,544,517).

Please note that the effective filing date for the pending claims is September 12, 2000, which is the date the full amino acid sequence of SEQ ID NO: 2 was first disclosed. SEQ ID NO: 2 was first disclosed in 09/660,587 filed September 12, 2000.

Rikihisa et al discloses the claimed amino acid and nucleic acid sequences as set forth in claimed SEQ ID NO: 42 and 41 respectively. SEQ ID NO: 48 and 47 as the same as Applicants' SEQ ID NO: 42 and 47 respectively (see sequence listing in issued patent).

8. Claim 1 is rejected under 35 U.S.C. 102(b) as being anticipated by Rikihisa et al (WO 99/13720), Ohashi et al Infection and Immunity, 1998 or Reddy et al BBRC, 1998.

Rikihisa et al (WO 98/13720), for example, discloses claimed an amino acid sequence of SEQ ID NO: 42. The prior art discloses a 82% sequence match with the claimed SEQ ID NO: 42 (claim 12 and figure 4B). See sequence search result printouts attached.

9. Claims 1 and 2 are rejected under 35 U.S.C. 102(b) as being anticipated by Ohashi et al J. Clinical Microbiology 1998.

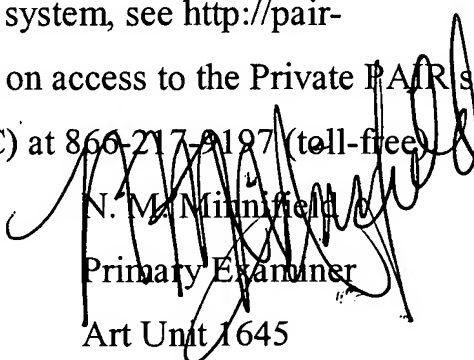
Ohashi et al discloses the claimed amino acid and nucleic acid sequences as set forth in claimed SEQ ID NO: 42 and 41 respectively, please see attached sequence search result printout.

10. Claims 1 and 2 are rejected under 35 U.S.C. 101 because the claimed invention is directed to non-statutory subject matter. Claims 1 and 2, as written, do not sufficiently distinguish over nucleic acids, and proteins as they exist naturally because the claims do not particularly point out any non-naturally occurring differences between the claimed products and the naturally occurring products. In the absence of the hand of man, the naturally occurring products are considered non-statutory subject matter. See *Diamond v. Chakrabarty*, 447 U.S. 303, 206 USPQ 193 (1980). The claims should be amended to indicate the hand of the inventor, e.g., by insertion of "Isolated" or "Purified" as taught and enabled in the specification. See MPEP 2105.

11. No claims are allowed.
12. The prior art made of record and not relied upon is considered pertinent to applicant's disclosure.
13. Any inquiry concerning this communication or earlier communications from the examiner should be directed to N. M. Minnifield whose telephone number is 571-272-0860. The examiner can normally be reached on M-F (8:00-5:30) Second Friday Off.

If attempts to reach the examiner by telephone are unsuccessful, the examiner's supervisor, Lynette R.F. Smith can be reached on 571-272-0864. The fax phone number for the organization where this application or proceeding is assigned is 703-872-9306.

Information regarding the status of an application may be obtained from the Patent Application Information Retrieval (PAIR) system. Status information for published applications may be obtained from either Private PAIR or Public PAIR. Status information for unpublished applications is available through Private PAIR only. For more information about the PAIR system, see <http://pair-direct.uspto.gov>. Should you have questions on access to the Private PAIR system, contact the Electronic Business Center (EBC) at 866-217-9197 (toll-free).


N. M. Minnifield
Primary Examiner
Art Unit 1645

NMM

March 21, 2005

Please mail w/ Action
3/21/05 MM

Feb 22 10:18:07 2005

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 17, 2005, 16:47:35 ; Search time 178 Seconds

(without alignments)
805.518 Million cell updates/sec

Title: US-10-680-349-42

Sequence: 1 MNYKKILVRSALISLMSILP.....ASVTLVDYGFGEIGMRFTF 280

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 segs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seg length: 0
Maximum DB seg length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database: UniProt_03.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1462	100.0	280	2	Q9F476
2	1452	99.3	280	2	Q84HU1
3	1224.5	83.8	283	2	Q8G8D6
4	1217.5	83.3	283	2	Q8G8I2
5	1217.5	83.3	283	2	Q8G8I2
6	1202.5	82.3	283	2	Q8G8I2
7	1124	76.9	282	2	Q9R443
8	1120	76.6	282	2	Q9R443
9	983	67.2	250	2	Q8VTT7
10	665.5	45.5	275	2	Q93DD4
11	655	44.8	276	2	Q8G8I0
12	651	44.3	276	2	Q8G8I7
13	648	44.3	280	2	Q9ZGM9
14	647	44.2	276	2	Q93DD1
15	645.5	44.2	281	2	Q93DD2
16	644.5	44.1	281	2	Q9ACI9
17	644	44.0	280	2	Q8S8I6
18	628	43.0	280	2	Q93DD3
19	621	42.5	288	2	Q9ZGJ2
20	620	42.4	286	2	Q52105
21	605	41.4	280	2	Q52107
22	605	41.4	291	2	Q8G8P3
23	601	41.1	280	2	Q9ADV3
24	600	41.0	280	2	Q9F473
25	599	41.0	291	2	Q8G921
26	598	40.9	291	2	Q8G8G2
27	592	40.5	285	2	Q916Y5
28	589	40.3	287	2	Q8G8G3
29	588	40.2	278	2	Q9R3J3
30	588	40.2	278	2	Q9R8A5
31	588	40.2	278	2	Q9R8A6

32	588	40.2	278	2	Q9R8A7	Q9R8A7 ehrlichia c
33	588	40.2	278	2	Q9R8A8	Q9R8A8 ehrlichia c
34	588	40.2	278	2	Q9R8A9	Q9R8A9 ehrlichia c
35	588	40.2	307	2	Q9ZGJ1	Q9ZGJ1 ehrlichia c
36	583.5	39.9	277	2	Q8G8W7	Q8G8W7 ehrlichia c
37	583.5	39.9	277	2	Q8G8W7	Q8G8W7 ehrlichia c
38	583	39.9	278	2	Q52106	Q52106 ehrlichia c
39	583	39.9	278	2	Q9F472	Q9F472 ehrlichia c
40	573.5	39.2	279	2	Q8G8O1	Q8G8O1 ehrlichia c
41	573	39.2	278	2	Q8G8O5	Q8G8O5 ehrlichia c
42	569	38.9	280	2	Q8G8C3	Q8G8C3 ehrlichia c
43	567.5	38.8	281	2	Q9S6H1	Q9S6H1 ehrlichia c
44	567	38.8	290	2	Q463J3	Q463J3 cowdria rum
45	566.5	38.7	271	2	Q69197	Q69197 ehrlichia c

ALIGNMENTS

RESULT 1	ID	Q9F476	PRELIMINARY;	PRT;	280 AA.
AC	Q9F476	Q9F476			
DT	01-MAR-2001	(TREMBLrel. 16, Created)			
DT	01-MAR-2001	(TREMBLrel. 16, Last sequence update)			
DT	05-JUL-2004	(TREMBLrel. 27, Last annotation update)			
DE	P28-2	(Major outer membrane protein P30-10).			
GN	Name=p28-2; Synonyms=p30-10;				
OS	Ehrlichia canis.				
OC	Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales;				
OC	Anaplasmataceae; Ehrlichia.				
OX	NCBI_TaxID=944;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=Jake;				
RX	MEDLINE=9242757; PubMed=10225842;				
RA	McBride J.W., Yu X.J., Walker D.H.;				
RT	"Cloning and characterization of multigene encoding the				
RT	28-kilodalton protein of Ehrlichia canis: a potential serodiagnostic				
RT	antigen.";				
RL	Clin. Diagn. Lab. Immunol. 6:392-399(1999).				
RN	[2]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=Oklaoma;				
RX	MEDLINE=9837112; PubMed=9705412;				
RA	Ohashi N., Unver A., Zhi N., Rikihisa Y.;				
RT	"Cloning and characterization of multigene encoding the				
RT	immunodominant 30-kilodalton major outer membrane proteins of				
RT	Ehrlichia canis and application of the recombinant protein for				
RT	serodiagnosis.";				
RL	J. Clin. Microbiol. 36:2671-2680(1998).				
RN	[4]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=Oklaoma;				
RX	MEDLINE=2153566; PubMed=11254561;				
RA	DOI=10.1128/IAI.69.4.2083-2091.2001;				
RT	Ohashi N., Rikihisa Y., Unver A.;				
RT	"Analysis of transcriptionally active gene clusters of major outer				
RT	membrane protein multigene family in Ehrlichia canis and E.				
RT	chaffeensis.";				
RL	Infect. Immun. 69:2083-2091(2001).				
RN	[5]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=Arizona, California, New Mexico, and Venezuela;				
RX	MEDLINE=22461952; PubMed=12574308;				

RA Felek S., Greene R., Rikhtsa Y.;
RT "Transcriptional Analysis of p30 Major Outer Membrane Protein Genes of
RT Ehrlichia canis in Naturally Infected Ticks and Sequence Analysis of
RT p30-10 of E. canis from Diverse Geographic Regions";
RL J. Clin. Microbiol. 41:886-888 (2003).
DR EMBL: AF082744; AAC14357.1; -
DR EMBL: AF078553; AAC8696.1; -
DR EMBL: AF324792; AAC1312.1; -
DR EMBL: AF528512; AAC1108.1; -
DR EMBL: AF528512; AAC1108.1; -
DR EMBL: AF528514; AAC1111.1; -
DR EMBL: AF528515; AAC1112.1; -
DR InterPro: IPR002566; Surface_Ag_mep4.
DR Pfam: PF01617; Surface_Ag_2; 1.
SQ SEQUENCE 280 AA; 30962 MW; D1B8285AF0B6CA3 CRC64;

Query Match 100.0%; Score 1462; DB 2; Length 280;
Best Local Similarity 100.0%; Pred. No. 7.9e-109;
Matches 280; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MNYKKILVRSALISLMSILPYOSFADPVGSRTNDNKEGFYISAKYNPSISHRKFSAEET 60
DB 1 MNYKKILVRSALISLMSILPYOSFADPVGSRTNDNKEGFYISAKYNPSISHRKFSAEET 60
QY 61 PINGTSLTKKVFGLKKDGDITRKODFTFVAPGIDFONNLISGFGSGISYMDGPRILE 120
DB 61 PINGTSLTKKVFGLKKDGDITRKODFTFVAPGIDFONNLISGFGSGISYMDGPRILE 120
QY 121 AAYQGFNPKNNTNDNDEEYKHPALSRKDMEDQOYVVLKNDGITFMSLWNTCYDIT 180
DB 121 AAYQGFNPKNNTNDNDEEYKHPALSRKDMEDQOYVVLKNDGITFMSLWNTCYDIT 180
QY 181 AEGVSFVYPACAGIGADLITTFKDLNLKFAVQKIGISYPIPEVSARFSGYHGVITGNK 240
DB 181 AEGVSFVYPACAGIGADLITTFKDLNLKFAVQKIGISYPIPEVSARFSGYHGVITGNK 240
QY 241 FEKIPVITPVVLANDPOTTSASVTLVDVGFGEIGMRFTF 280
DB 241 FEKIPVITPVVLANDPOTTSASVTLVDVGFGEIGMRFTF 280

RESULT 2
Q84HU1 PRELIMINARY; PRT; 280 AA.
AC 084HU1;
DT 01-JUN-2003 (TREMBlrel. 24, Created)
DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Major outer membrane protein.
GN Namep30-10.
OS Ehrlichia canis.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales;
OC Anaplasmataceae; Ehrlichia.
OX NCBI_TaxID=944;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=Hawaii;
RX MEDLINE=22461952; PubMed=12574308;
RA Felek S., Greene R., Rikhtsa Y.;
RT "Transcriptional Analysis of p30 Major Outer Membrane Protein Genes of
RT Ehrlichia canis in Naturally Infected Ticks and Sequence Analysis of
RT p30-10 of E. canis from Diverse Geographic Regions";
RL J. Clin. Microbiol. 41:886-888 (2003).
DR EMBL: AF528513; AAC1110.1; -
DR InterPro: IPR002566; Surface_Ag_mep4.
DR Pfam: PF01617; Surface_Ag_2; 1.
SQ SEQUENCE 280 AA; 30990 MW; D1B828B14F5BDC2 CRC64;

Query Match 99.3%; Score 1452; DB 2; Length 280;
Best Local Similarity 99.3%; Pred. No. 5e-108;
Matches 278; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
1 MNYKKILVRSALISLMSILPYOSFADPVGSRTNDNKEGFYISAKYNPSISHRKFSAEET 60

DB 1 MNYKKILVRSALISLMSILPYOSFADPVGSRTNDNKEGFYISAKYNPSISHRKFSAEET 60
QY 61 PINGTSLTKKVFGLKKDGDITRKODFTFVAPGIDFONNLISGFGSGISYMDGPRILE 120
DB 61 PINGTSLTKKVFGLKKDGDITRKODFTFVAPGIDFONNLISGFGSGISYMDGPRILE 120
QY 121 AAYQGFNPKNNTNDNDEEYKHPALSRKDMEDQOYVVLKNDGITFMSLWNTCYDIT 180
DB 121 AAYQGFNPKNNTNDNDEEYKHPALSRKDMEDQOYVVLKNDGITFMSLWNTCYDIT 180
QY 181 AEGVSFVYPACAGIGADLITTFKDLNLKFAVQKIGISYPIPEVSARFSGYHGVITGNK 240
DB 181 AEGVSFVYPACAGIGADLITTFKDLNLKFAVQKIGISYPIPEVSARFSGYHGVITGNK 240
QY 241 FEKIPVITPVVLANDPOTTSASVTLVDVGFGEIGMRFTF 280
DB 241 FEKIPVITPVVLANDPOTTSASVTLVDVGFGEIGMRFTF 280

RESULT 3
Q8GBD6 PRELIMINARY; PRT; 283 AA.
ID 08GBD6;
AC 08GBD6;
DT 01-MAR-2003 (TREMBlrel. 23, Created)
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE 28kDa outer membrane protein gene 14.
OS Ehrlichia chaffeensis.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales;
OC Anaplasmataceae; Ehrlichia.
OX NCBI_TaxID=945;
RN (1)
RP SEQUENCE FROM N.A.
RC MEDLINE=22384137; PubMed=12496165; DOI=10.1128/IAI.71.1.187-195.2003;
RA Cheng C., Paddock C.D., Ganta R.R.;
RT "Molecular heterogeneity of Ehrlichia chaffeensis isolates determined
RT by sequence analysis of the 28-kilodalton outer membrane protein genes
RT and other regions of the genome";
RL Infect. Immun. 71:187-195 (2003).
DR EMBL: AF479835; AAC12939.1; -
DR EMBL: AF479836; AAC12944.1; -
DR EMBL: AF479838; AAC12954.1; -
DR InterPro: IPR002566; Surface_Ag_mep4.
DR Pfam: PF01617; Surface_Ag_2; 1.
SQ SEQUENCE 283 AA; 31090 MW; D5825DD4DC51C425 CRC64;

Query Match 83.8%; Score 1224.5; DB 2; Length 283;
Best Local Similarity 81.6%; Pred. No. 8e-90;
Matches 231; Conservative 24; Mismatches 25; Indels 3; Gaps 1;

QY 1 MNYKKILVRSALISLMSILPYOSFADPVGSRTNDNKEGFYISAKYNPSISHRKFSA 57
DB 1 MNYKKILVRSALISLMSILPYOSFADPVGSRTNDNKEGFYISAKYNPSISHRKFSA 60
QY 58 EETPINGTSLTKKVFGLKKDGDITRKODFTFVAPGIDFONNLISGFGSGISYMDGPRILE 117
DB 58 EETPINGTSLTKKVFGLKKDGDITRKODFTFVAPGIDFONNLISGFGSGISYMDGPRILE 120
QY 118 EIEAAYQGFNPKNNTNDNDEEYKHPALSRKDMEDQOYVVLKNDGITFMSLWNTCY 177
DB 118 EIEAAYQGFNPKNNTNDNDEEYKHPALSRKDMEDQOYVVLKNDGITFMSLWNTCY 180
QY 178 DITAEVSFVYPACAGIGADLITTFKDLNLKFAVQKIGISYPIPEVSARFSGYHGVITGNK 240
DB 178 DITAEVSFVYPACAGIGADLITTFKDLNLKFAVQKIGISYPIPEVSARFSGYHGVITGNK 240
QY 238 GNEKEKIPVITPVVLANDPOTTSASVTLVDVGFGEIGMRFTF 280
DB 238 GNEKEKIPVITPVVLANDPOTTSASVTLVDVGFGEIGMRFTF 283

RESULT 4

W

W

✱ ✱ ✕

[illegible]

pld. mail w/ action
3/2/05 mm

RX DOI=10.1128/IAI.69.4.2083-2091.2001;
 RA Ohashi N., Rikihisa Y., Unver A.;
 RT "Analysis of transcriptionally active gene clusters of major outer
 membrane protein multigene family in *Escherichia coli* and *E.*
 RT *coli* strains."
 RT Infect. Immun. 69:2083-2091(2001).
 DR EMBL; AF479833; AAC02936.1; -.
 DR EMBL; AF479834; AAC02933.1; -.
 DR InterPro: IPR002566; Surface_Ag_map4.
 DR Pfam: PF01617; Surface_Ag_2; 1.
 SQ SEQUENCE 283 AA; 31017 MW; DCBCE528771C95D CRC64;

Query Match 82.3%; Score 1202.5; DB 2; Length 283;
 Best Local Similarity 79.5%; Pred. No. 4.6e-88;
 Matches 225; Conservative 26; Mismatches 29; Indels 3; Gaps 1;

QY 1 MNYKKILVRSALISLMSILPYQSFADPVGSR--TNDKSGFYISAKNPSISHFRKFS 57
 DB 1 MNYKKILVRSALISLMSILPYQSFADPVGSR--TNDKSGFYISAKNPSISHFRKFS 60
 QY 58 EETPINGNSLTKKVFGKKGDDITKDDPTFVAAGIDFONNLISGFSGISGMDGPR 117
 DB 61 EETPINGNSLTKKVFGKKGDDITKDDPTFVAAGIDFONNLISGFSGISGMDGPR 120
 QY 118 ELBAAYQGFNPKNTDNDNGEYRGHGFALSRDAMDOQYVVLKNDGTFMSLMVNTCY 177
 DB 121 ELBAAYQGFNPKNTDNDNGEYRGHGFALSRDAMDOQYVVLKNDGTFMSLMVNTCY 180
 QY 178 DITAEVGFVPAACAGIGADLITFQDLNLFKPAVQKIGISYPTPEVSATIGYHGV 237
 DB 181 DITAEVGFVPAACAGIGADLITFQDLNLFKPAVQKIGISYPTPEVSATIGYHGV 240
 QY 238 GNFKEKIPVITPVVNDAPQTTASVTLVGVFGSGISGRFTF 280
 DB 241 GNFKEKIPVITPVVNDAPQTTASVTLVGVFGSGISGRFTF 283

RESULT 7

QY 09R443 PRELIMINARY; PRT; 282 AA.
 AC 09R443;
 DT 01-MAY-2000 (Tremblrel. 13, Created)
 DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
 DT 05-JUL-2004 (Tremblrel. 27, Last annotation update)
 DE Major antigenic protein 1 like protein.
 OS *Cowdria ruminantium*.
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales;
 OC Anaplasmataceae; Ehrlichia.
 NCBI_TaxID=779;

RP SEQUENCE FROM N.A.
 RA MEDLINE=99216274; PubMed=10198207; DOI=10.1006/dbrc.1999.0459;
 RA Salsosa C.R., Mahan S.M., Barber A.F.;
 RT "The map1 gene of *Cowdria ruminantium* is a member of a multigene
 RT family containing both conserved and variable genes."
 RT Biochem. Biophys. Res. Commun. 257:300-305(1999).
 DR EMBL; AF125274; AAD26343.1; -.
 DR EMBL; AF125277; AAD26349.1; -.
 DR EMBL; AF125278; AAD26351.1; -.
 DR InterPro: IPR002566; Surface_Ag_map4.
 DR Pfam: PF01617; Surface_Ag_2; 1.
 SQ SEQUENCE 282 AA; 31040 MW; 0CB3C65775C8C90 CRC64;

Query Match 76.9%; Score 1124; DB 2; Length 282;
 Best Local Similarity 76.0%; Pred. No. 8.7e-82;
 Matches 215; Conservative 26; Mismatches 38; Indels 4; Gaps 3;

QY 1 MNYKKILVRSALISLMSILPYQSFADPVGSR--NDN-KEGYISAKNPSISHFRKFS 57
 DB 1 MNYKKILVRSALISLMSILPYQSFADPVGSR--NDN-KEGYISAKNPSISHFRKFS 60

QY 58 EETPINGNSLTKKVFGKKGDDITKDDPTFVAAGIDFONNLISGFSGISGMDGPR 117
 DB 61 EETPINGNSLTKKVFGKKGDDITKDDPTFVAAGIDFONNLISGFSGISGMDGPR 120
 QY 118 ELBAAYQGFNPKNTDNDNGEYRGHGFALSRDAMDOQYVVLKNDGTFMSLMVNTCY 177
 DB 121 ELBAAYQGFNPKNTDNDNGEYRGHGFALSRDAMDOQYVVLKNDGTFMSLMVNTCY 179
 QY 178 DITAEVGFVPAACAGIGADLITFQDLNLFKPAVQKIGISYPTPEVSATIGYHGV 237
 DB 180 DITAEVGFVPAACAGIGADLITFQDLNLFKPAVQKIGISYPTPEVSATIGYHGV 239
 QY 238 GNFKEKIPVITPVVNDAPQTTASVTLVGVFGSGISGRFTF 280
 DB 240 GNFKEKIPVITPVVNDAPQTTASVTLVGVFGSGISGRFTF 282

RESULT 8

QY 09M41 PRELIMINARY; PRT; 282 AA.
 AC 09M41;
 DT 01-NOV-1999 (Tremblrel. 12, Created)
 DT 01-NOV-1999 (Tremblrel. 12, Last sequence update)
 DT 05-JUL-2004 (Tremblrel. 27, Last annotation update)
 DE Major antigenic protein 1 like protein (MAP1-1).
 OS *Cowdria ruminantium*.
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales;
 OC Anaplasmataceae; Ehrlichia.
 NCBI_TaxID=779;

RP SEQUENCE FROM N.A.
 RA MEDLINE=99216274; PubMed=10198207; DOI=10.1006/dbrc.1999.0459;
 RA Salsosa C.R., Mahan S.M., Barber A.F.;
 RT "The map1 gene of *Cowdria ruminantium* is a member of a multigene
 RT family containing both conserved and variable genes."
 RT Biochem. Biophys. Res. Commun. 257:300-305(1999).
 DR EMBL; AF125274; AAD26343.1; -.
 DR EMBL; AF125277; AAD26349.1; -.
 DR EMBL; AF125278; AAD26351.1; -.
 DR InterPro: IPR002566; Surface_Ag_map4.
 DR Pfam: PF01617; Surface_Ag_2; 1.
 SQ SEQUENCE 282 AA; 31100 MW; 1CB2DA256B2CA990 CRC64;

Query Match 76.6%; Score 1120; DB 2; Length 282;
 Best Local Similarity 75.6%; Pred. No. 1.8e-81;
 Matches 214; Conservative 26; Mismatches 39; Indels 4; Gaps 3;

QY 1 MNYKKILVRSALISLMSILPYQSFADPVGSR--NDN-KEGYISAKNPSISHFRKFS 57
 DB 1 MNYKKILVRSALISLMSILPYQSFADPVGSR--NDN-KEGYISAKNPSISHFRKFS 60
 QY 58 EETPINGNSLTKKVFGKKGDDITKDDPTFVAAGIDFONNLISGFSGISGMDGPR 117
 DB 61 EETPINGNSLTKKVFGKKGDDITKDDPTFVAAGIDFONNLISGFSGISGMDGPR 120
 QY 118 ELBAAYQGFNPKNTDNDNGEYRGHGFALSRDAMDOQYVVLKNDGTFMSLMVNTCY 177
 DB 121 ELBAAYQGFNPKNTDNDNGEYRGHGFALSRDAMDOQYVVLKNDGTFMSLMVNTCY 179
 QY 178 DITAEVGFVPAACAGIGADLITFQDLNLFKPAVQKIGISYPTPEVSATIGYHGV 237
 DB 180 DITAEVGFVPAACAGIGADLITFQDLNLFKPAVQKIGISYPTPEVSATIGYHGV 239
 QY 238 GNFKEKIPVITPVVNDAPQTTASVTLVGVFGSGISGRFTF 280

RESULT 2	AR303107	AR303107	843 bp	DNA	linear	PAT 12-JUN-2003
LOCUS	AR303107					
DEFINITION	Sequence 47 from patent US 6544517.					
ACCESSION	AR303107					
VERSION	AR303107.1	GI:31691747				
KEYWORDS						
SOURCE	Unknown.					
ORGANISM	Unknown.					

REFERENCE	AUTHORS	TITLE	JOURNAL	FRATUTES	SOURCE
Unclassified.					
1 (Pages 1 to 843)	Rikhtsa, Y. and Ohashi, N.	Outer membrane protein of <i>Escherichia</i> canis and <i>Escherichia</i> <i>Chaffensis</i>	Patent: US 6544517-A	47 08-APR-2003;	
		Location/Qualifiers			
		1. .843			

```
/organism="unknown"  
/mol_type="genomic DNA"
```

Query Match	100.0%	Score 840;	DB 6;	Length 843;
Best Local Similarity	100.0%	Pred. No. 3,1e-140;		
Matches 840;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0
QY	1	ATGAAATTATAGAAAATTCCTAGTATAGAAAGCGGGCTTAATCTGATTATATGTCATCTTACCA	60	
Db	1	ATGAATATATAGAAAATTCCTAGTATAGAAAGCGGGCTTAATCTATATATGTCATCTTACCA	60	
QY	61	TATACGCTTTTGCAGATCCTGTAGGTTCAAGAACTAATGATTAACAAGAGGCTTAC	120	
Db	61	TATACGCTTTTGCAGATCCTGTAGGTTCAAGAACTAATGATTAACAAGAGGCTTAC	120	
QY	121	ATTAGTCAAAAGTACATCCAAATATATCAACCTTAGAAAATCTCTGCTGAAGAAACT	180	

D	b	121	ATTAGTGAAGTACAAATCCAAAGTATTCACACTTTGAAAAATTCCTCGTGAAGAACT	18
Q	y	181	CCATTTAATGGACAAATTCCTGACATPAAAAAGTTTCCGACATPAAAGAAATGGTGAT	24
D	b	181	CCATTTAATGGACAAATTCCTGACATPAAAAAGTTTCCGACATPAAAGAAATGGTGAT	24
Q	y	241	ATAACAAAAAAGCCGATTTTACAGAGTAgCTCCAGGCAATGATTTTCAAAATAACTTA	30
D	b	241	ATAACAAAAAAGCCGATTTTACAGAGTAgCTCCAGGCAATGATTTTCAAAATAACTTA	30
Q	y	301	ATATCAGATTTTCAAGAGTATGGTTACTATGACGACCAAGATPAACTTGAA	36
D	b	301	ATATCAGATTTTCAAGAGTATGGTTACTATGACGACCAAGATPAACTTGAA	36
Q	y	361	GCATCATATCAACATTTAATCCAAAAAACCCGATPACATGATATCTGATTAATGGTGA	42
D	b	361	GCATCATATCAACATTTAATCCAAAAAACCCGATPACATGATATCTGATTAATGGTGA	42
Q	y	421	TACTATPAAACATTTGSCATTAATCCTGTAAGATGCAATGAGATGCAATATGTAGTA	48
D	b	421	TACTATPAAACATTTGSCATTAATCCTGTAAGATGCAATGAGATGCAATATGTAGTA	48
Q	y	481	CTTAAAAAATGACGGCATPACTTTTATGTCATGATGGTTAATATCTTGATATGACATTAC	54
D	b	481	CTTAAAAAATGACGGCATPACTTTTATGTCATGATGGTTAATATCTTGATATGACATTAC	54
Q	y	541	GCGAAGAGTATCTTGGTACATATGCAATGCAATGCAAGGAAAAATAGTATTAACCTT	60
D	b	541	GCGAAGAGTATCTTGGTACATATGCAATGCAATGCAAGGAAAAATAGTATTAACCTT	60
Q	y	601	ATTTTAAAGACCTGATCTAAATTTTGCTTACCAAGGAAAAATAGTATTAACCTT	66
D	b	601	ATTTTAAAGACCTGATCTAAATTTTGCTTACCAAGGAAAAATAGTATTAACCTT	66
Q	y	661	ATCACAACAGAAAGTCTTCGCAATTAATGGTGATATCTACATAGGCGTTATGGTAAATAA	72
D	b	661	ATCACAACAGAAAGTCTTCGCAATTAATGGTGATATCTACATAGGCGTTATGGTAAATAA	72
Q	y	721	TTTGAGAGATPACCTGTATAACCTCGTAAATAATAATGATGCTCTCAAAACAACATCT	78
D	b	721	TTTGAGAGATPACCTGTATAACCTCGTAAATAATAATGATGCTCTCAAAACAACATCT	78
Q	y	781	GCTTCAAGTAACTCTTGACGTTGATATCTTTGGCGGAGAAATGGAAATGAGGTTACCTTC	84
D	b	781	GCTTCAAGTAACTCTTGACGTTGATATCTTTGGCGGAGAAATGGAAATGAGGTTACCTTC	84

RESULT 3					
AF528511					
LOCUS					
DEFINITION	AF528511	906 bp	DNA	linear	BCT 14-PEB-2002
ACCESSION	Ehrlichia canis strain Arizona major outer membrane protein				
VERSION	(p30-10) gene, complete cds.				
KEYWORDS	AF528511				
SOURCE	AF528511.1	GI:28376378			
ORGANISM	Ehrlichia canis				
	Ehrlichia canis				
	Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales;				
	Anaplasmataceae; Ehrlichia.				
REFERENCE	1 (bases 1 to 906)				
AUTHORS	Felak,S., Greene,R. and Rikhisa,Y.				
TITLE	Transcriptional Analysis of p30 Major Outer Membrane Protein Genes of Ehrlichia canis in Naturally Infected Ticks and Sequence Analysis of p30-10 of E. canis from Diverse Geographic Regions J. Clin. Microbiol. 41 (2), 886-888 (2003)				
JOURNAL	MEDLINE				
PUBMED	22461952				
REFERENCE	12574308				
AUTHORS	2 (bases 1 to 906)				
TITLE	Felak,S., Greene,R. and Rikhisa,Y.				
JOURNAL	Direct Submission				
	Submitted (12-JUL-2002) Veterinary Biodefence Unit				

University, 1900 Coffey Road, Columbus, OH 43210, USA

ple. mail w action
3/2/05
m

QY 661 ATCACACGAGAGTCTGCACTTATTTGGTGAATACCAATGCGCTTATTTGTAATAA 720
DB 661 ATGACACGAGAGTCTGCACTTATTTGGTGAATACCAATGCGCTTATTTGTAATAA 720
QY 721 TTGAGAGAGTATCTGTAATTAATCTCTGTAGTATTAATGATGCTCTCAACCAATCT 780
DB 721 TTGAGAGAGTATCTGTAATTAATCTCTGTAGTATTAATGATGCTCTCAACCAATCT 780
QY 781 GCTTCAGTAACTCTTGAAGTGTGATGATGCGGAGAAATTTGGAATGAGGTTCACTTC 840
DB 781 GCTTCAGTAACTCTTGAAGTGTGATGATGCGGAGAAATTTGGAATGAGGTTCACTTC 840

RESULT 6
AF528515 906 bp DNA linear BCT 14-FEB-2003
DEFINITION Ehrlichia canis strain Venezuela major outer membrane protein (p30-10) gene, complete cds.
ACCESSION AF528515
VERSION AF528515.1 GI:28376386
KEYWORDS
SOURCE
ORGANISM Ehrlichia canis
Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales; Anaplasmataceae; Ehrlichia.
REFERENCE
AUTHORS 1 (bases 1 to 906)
TITLE Pelek, S., Greene, R. and Rikihisa, Y.
JOURNAL Transcriptional Analysis of p30 Major Outer Membrane Protein Genes of Ehrlichia canis in Naturally Infected Ticks and Sequence Analysis of p30-10 of E. canis from Diverse Geographic Regions
MEDLINE J. Clin. Microbiol. 41 (2), 886-888 (2003)
PUBMED 22461952
2 (bases 1 to 906)
12574308
REFERENCE
AUTHORS Felek, S., Greene, R. and Rikihisa, Y.
JOURNAL Direct Submission
TITLE Submitted (12-JUL-2002) Veterinary Biosciences, Ohio State University, 1900 Coffey Road, Columbus, OH 43210, USA
FEATURES
source location/Qualifiers
1. .906
/organism="Ehrlichia canis"
/mol_type="genomic DNA"
/strain="Venezuela"
/db_xref="taxon:944"
1. .843
/gene="p30-10"
1. .843
/gene="p30-10"
/note="p30-10"
/codon_start=1
/transl_table=1
/product="major outer membrane protein"
/protein_id="AA04112.1"
/db_xref="GI:28376386"
/translation="MNYKKILVRSALISLSILPYGSPADPVGSRTNDNKEGYISAK YNBSISHRFKRSABETPINDGNSLTKVFGIKKQDITKDDPFRVAPGIDPQNNLIS GPSSIGSYMDGPRIELBAAYQCFNPKNDDNDNEKYHFLSKMDQDOYV LKNDGITFMSLMVNTCYDITAEVSPFVYACAGIGALITIPQINKKPYOGKIGIS YPTPEVSATIGGYTHGVIGNKPKIKIVITPVVANDAPQTTASVTLLDVGFGSEIGM RFTF"

ORIGIN
Query Match 100.0%; Score 840; DB 1; Length 906;
Best Local Similarity 100.0%; Pred. No. 3, 1e-140; Indels 0; Gaps 0;
Matches 840; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAATTAATGAAGAAATTTGTAAGAGCGGCTTAATCTATTAATGTCATCTTACCA 60
DB 1 ATGAATTAATGAAGAAATTTGTAAGAGCGGCTTAATCTATTAATGTCATCTTACCA 60
QY 61 TATCAGCTTTTGGAGATCTCTGTAGTCAAGAACTAATGATTAACAAAGAGGCTTAC 120
DB 61 TATCAGCTTTTGGAGATCTCTGTAGTCAAGAACTAATGATTAACAAAGAGGCTTAC 120

QY 121 ATTAGTCAAGATGACATCCAGTATATCACTTTAGAAAATTCCTGCTGAGAAACT 180
DB 121 ATTAGTCAAGATGACATCCAGTATATCACTTTAGAAAATTCCTGCTGAGAAACT 180
QY 181 CCTATTAAATGGAACAAATTCCTGCTACTTAAAAAGTTTGGACTAAAGAAAGTGTAT 240
DB 181 CCTATTAAATGGAACAAATTCCTGCTACTTAAAAAGTTTGGACTAAAGAAAGTGTAT 240
QY 241 ATAAACAAAAAGAGATTTTCAAGAGTAGCTCCAGGATGATTTTCAAAATACTTA 300
DB 241 ATAAACAAAAAGAGATTTTCAAGAGTAGCTCCAGGATGATTTTCAAAATACTTA 300
QY 301 ATATCAGATTTTCAAGAGTATTTGTTACTATGACGACCAAGAAATAGAACTTGA 360
DB 301 ATATCAGATTTTCAAGAGTATTTGTTACTATGACGACCAAGAAATAGAACTTGA 360
QY 361 GCTGCATATCAACATTTATTCGAAAAACCCGATACAAATGATCTGATTAATGTTGA 420
DB 361 GCTGCATATCAACATTTATTCGAAAAACCCGATACAAATGATCTGATTAATGTTGA 420
QY 421 TACTATTAACATTTGATTCATTCCTGTAAGATGCAATGAGATCAGATATGATGA 480
DB 421 TACTATTAACATTTGATTCATTCCTGTAAGATGCAATGAGATCAGATATGATGA 480
QY 481 CTTAAATAATGACCGCATTAATTTATGTCATGATGATGATTAATCTGATGATTA 540
DB 481 CTTAAATAATGACCGCATTAATTTATGTCATGATGATGATTAATCTGATGATTA 540
QY 541 GCTGAAGAGATATCTTGTGATCATATGATGATGATGATGATGATGATGATGAT 600
DB 541 GCTGAAGAGATATCTTGTGATCATATGATGATGATGATGATGATGATGATGAT 600
QY 601 ATTTTAAAGACTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 660
DB 601 ATTTTAAAGACTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 660
QY 661 ATGACACGAGAGTCTGCACTTATTTGGTGAATACCAATGCGCTTATTTGTAATAA 720
DB 661 ATGACACGAGAGTCTGCACTTATTTGGTGAATACCAATGCGCTTATTTGTAATAA 720
QY 721 TTGAGAGAGTATCTGTAATTAATCTCTGTAGTATTAATGATGCTCTCAACCAATCT 780
DB 721 TTGAGAGAGTATCTGTAATTAATCTCTGTAGTATTAATGATGCTCTCAACCAATCT 780
QY 781 GCTTCAGTAACTCTTGAAGTGTGATGATGCGGAGAAATTTGGAATGAGGTTCACTTC 840
DB 781 GCTTCAGTAACTCTTGAAGTGTGATGATGCGGAGAAATTTGGAATGAGGTTCACTTC 840

RESULT 7
AF324792 6913 bp DNA linear BCT 11-APR-2001
DEFINITION Ehrlichia canis phosphoribosylaminimidazole carboxylase (purK) gene, complete cds; major outer membrane protein gene cluster 2, complete sequence; and u6 gene, partial cds.
ACCESSION AF324792
VERSION AF324792.1 GI:13591681
KEYWORDS
SOURCE
ORGANISM Ehrlichia canis
Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales; Anaplasmataceae; Ehrlichia.
REFERENCE
AUTHORS 1 (bases 1 to 6913)
TITLE Ohashi, N., Unver, A., Zhi, N. and Rikihisa, Y.
JOURNAL Cloning and characterization of multigenes encoding the immunodominant 30-kilodalton major outer membrane proteins of Ehrlichia canis and application of the recombinant protein for serodiagnosis
MEDLINE J. Clin. Microbiol. 36 (9), 2671-2680 (1998)
PUBMED 9705412
REFERENCE 2 (bases 1 to 6913)

AUTHORS	Osashi, N., Rikhiisa, Y. and Unver, A.
TITLE	Analyses of transcriptionally active gene clusters of major outer membrane protein multigene family in <i>Brachycauda</i> and <i>E. chaffeensis</i>
JOURNAL	<i>Infect. Immun.</i> 69 (4), 2083-2091 (2001)
MEDLINE	21153566
PUBMED	11254561
REFERENCE	3 (bases 1 to 6913)
AUTHORS	Osashi, N., Rikhiisa, Y. and Unver, A.
TITLE	Direct Submission
JOURNAL	Submitted (29-NOV-2000) Veterinary Biosciences, Ohio State University, 1925 Coffey Rd., Columbus, OH 43210, USA
FEATURES	Location/Qualifiers
source	1..6913

/product="major outer membrane protein P30a"
 /protein_id="AAK31314.1"
 /db_xref="GI:13591685"
 /translation="MKKKTFTVALVLLSPTHFPSPSPASTINHPYISGKTM
 TASHLIFPAKEQSEFTKVLVGLDORLSNININNDTAKSLVQNSYSEFYKKNPLGAG
 AAGISGLNISRILEVSHSEIPDTQNPKNVYLNNDSHKCALSHGSHICSDGSGDMY
 ACTDQPVLLKNGSLDVSFLMACYDITTEKRPSPYICAGITDLISMFETORKIK
 YQKGLGNTTINSRVSFPAAGFPHKVIQNEFKGIPYLLPDGSGNIKVQSGATVTLVGC
 FELISGRFFP"
 complement(5309..*6913)
 /gene="u6"
 complement(5309..*6913)
 /complement(5309..*6913)
 /gene="u6"
 /codon_start=1
 /transl_table=1
 /product="unknown"
 /protein_id="AAK31315.1"
 /db_xref="GI:13591686"
 /translation="KLIIVTDKRVSDIIVHFGISIVRPKINPNDHOPVLYQNKDQKQ
 VLKDEFCODNAVGOIRYOHDDKVTYACIGINTTFEYVALKSHNVYDKHTWLKALPYND
 MVRVLVDKKOYICADYEYDITKNDOPDLSIINEDNTYFSDVEQHRKKLALYKDD
 DNPNCNKNSPYLOQNTKELKIDANKSTLTPPEVFTQFKSDSLNSNVEYNLKNOKLII
 SADMTKSYRFDTHVLAYEVNDNKEMSLDLPKQLBIQPLDHSNMGWCISFSEITVY
 PERKTESDKNPSALPLVQEDNKSEVTLIYPLSGSLYVNRKQDFIKVIMLGLGSGEG
 KIDIKSWIKGEQPGEYVMGFKKKSDKFKVATYFPRMKNKSEKSNDRHLKONSDV
 GMAVAIEFCCKDERLHDGEVCEVOLTANGGKQGHIRKAVKYSNNLVWDRMLYRYV
 NSHVSRSRENVPHDKRIREFIYQNPITLALMEIIEKDECKSGRLAENNSKYFGAGGC
 VVDSTSTERGAGMVKITCEDMYHE"

ORIGIN

Query Match	100.0%	Score 840;	DB 1;	Length 6913
Best Local Similarity	100.0%	Pred. NO	1	82.170.

Qy	1	ATGAATATATAGAAAAATTCTAGTAAAGAGCGCTTAATCTCATTTAATGTCAATCTTAAACA	60
Db	1756	ATGATATTAAGAAAAATTCATAGTAAAGCGCTTAATCTCATTTAATGTCAATCTTAAACA	181
Qy	61	TATCAGTCTTTGCAGATCCCTGTAAGTTCAGAACTTAATGATTAACAAGAGCTTCTAC	120
Db	1816	TATCAGTCTTTGCAGATCCCTGTAAGTTCAGAACTTAATGATTAACAAGAGCTTCTAC	187
Qy	121	ATTAGTCAAAAGTACATCCAGTATATCAACTTTAGAAAAATTCCTGCTGAAGAACT	180
Db	1876	ATTAGTCAAAAGTACATCCAGTATATCAACTTTAGAAAAATTCCTGCTGAAGAACT	193
Qy	181	CCATATTAAGCAACAATCTCTCACTAAAAAAAGTTTGGACTAAAGAAAGTGTGAT	240
Db	1936	CCATATTAAGCAACAATCTCTCACTAAAAAAAGTTTGGACTAAAGAAAGTGTGAT	199
Qy	241	ATAACAAAAAAGAGATTTTACAGAGTAGTCCAGCGATTTGATTTCAAAATACTTA	300
Db	1996	ATAACAAAAAAGAGATTTTACAGAGTAGTCCAGCGATTTGATTTCAAAATACTTA	205
Qy	301	ATATCAGGATTTTCAGAAAGTATGGTAACTCTATGAGCGGACCAAGATTTGAACTTGAA	360
Db	2056	ATATCAGGATTTTCAGAAAGTATGGTAACTCTATGAGCGGACCAAGATTTGAACTTGAA	2115
Qy	361	GCTGATATCAACAATTTAATCCAAAAACCGATTAACATGATCTGATTAATGTGTA	420
Db	2116	GCTGATATCAACAATTTAATCCAAAAACCGATTAACATGATCTGATTAATGTGTA	2175
Qy	421	TACTATTAACAATTTGGCATTAATCTCGTAAAGATGCCAATGGAAGATCAGCAATATGTGTA	480
Db	2176	TACTATTAACAATTTGGCATTAATCTCGTAAAGATGCCAATGGAAGATCAGCAATATGTGTA	2235
Qy	481	CTTAAAAATGACGGCAATCTTTATATGCTATGATGTTAATCTTGCTATGACATTACA	540
Db	2236	CTTAAAAATGACGGCAATCTTTATATGCTATGATGTTAATCTTGCTATGACATTACA	2295
Qy	541	GCTGAAGAGATATCTTTCGATACATATGCAATGCGAGGTATAGAGCAATCTTATCACT	600
Db	2296	GCTGAAGAGATATCTTTCGATACATATGCAATGCGAGGTATAGAGCAATCTTATCACT	2355

ple. mail of action
2/21/05 pm
page 7

QY 601 ATTTTAAGACCTCAATCTAATAATTTGCTTACCAAGAAAATAGTATTAGTACCCT 660
DB 2356 ATTTTAAGACCTCAATCTAATAATTTGCTTACCAAGAAAATAGTATTAGTACCCT 2415
QY 661 ATCAACACCAAGAGTCTGCAATTTATGATGATCTACTACATGGCGTATTGTTAATAA 720
DB 2416 ATCAACACCAAGAGTCTGCAATTTATGATGATCTACTACATGGCGTATTGTTAATAA 2475
QY 721 TTGAGAGAGATACCTGTAATAAATCTCTGTAGTATTAAATGATGCTCTCAACACATCT 780
DB 2476 TTGAGAGAGATACCTGTAATAAATCTCTGTAGTATTAAATGATGCTCTCAACACATCT 2535
QY 781 GCTTCAGTAATCTTGAAGTGTGATCTTTGGCCGAGAAATTTGCAATGAGTTCACTTC 840
DB 2536 GCTTCAGTAATCTTGAAGTGTGATCTTTGGCCGAGAAATTTGCAATGAGTTCACTTC 2595

RESULT 8
LOCUS AF082744 11329 bp DNA linear BCT 18-SEP-2000
DEFINITION Ehrlichia canis p28 multigene locus, partial sequence.
ACCESSION AF082744 AF168788 AF168789
VERSION AF082744.2 GI:10181081
KEYWORDS
SOURCE Ehrlichia canis
ORGANISM Ehrlichia canis
Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales; Anaplasmataceae; Ehrlichia.
REFERENCE 1 (bases 1 to 11329)
McBride, J.W., Yu, X.J. and Walker, D.H.
Molecular cloning of the gene for a conserved major immunoreactive 28-kilodalton protein of Ehrlichia canis: a potential serodiagnostic antigen
Clin. Diagn. Immunol. 6 (3), 392-399 (1999)
JOURNAL MEDLINE 99242757
PUBMED 10225842
REFERENCE 2 (bases 1 to 11329)
McBride, J.W., Yu, X.J. and Walker, D.H.
A conserved, transcriptionally active p28 multigene locus of Ehrlichia canis
Gene 254 (1-2), 245-252 (2000)
JOURNAL MEDLINE 20432107
PUBMED 10974556
REFERENCE 3 (bases 1 to 11329)
McBride, J.W., Yu, X.J. and Walker, D.H.
Direct Submission
Submitted (07-AUG-1998) Pathology, University of Texas Medical Branch, 301 University Blvd., Galveston, TX 77555-0609, USA
4 (bases 1 to 11329)
McBride, J.W., Yu, X.J. and Walker, D.H.
Direct Submission
Submitted (04-AUG-2000) Pathology, University of Texas Medical Branch, 301 University Blvd., Galveston, TX 77555-0609, USA
REMARK COMMENT
FEATURES
On Sep 18, 2000 this sequence version replaced gi:3769522.
Location/Qualifiers
1..11329
/organism="Ehrlichia canis"
/mol_type="genomic DNA"
/strain="Jake"
/db_xref="taxon:944"
<1..146
/gene="p28a"
<1..146
/gene="p28a"
/note="outer membrane protein"
/codon_start=3
/transl_table=11
/product="p28"
/protein_id="AA014355.1"
/db_xref="GI:10181081"
/translation="SIIISHYVKNLPIQYVNTLEPRVTSATATLDIGVLGEIGIR

gene 170..1051
CDS /gene="p28-1"
170..1051
/gene="p28-1"
/note="outer membrane protein"
/codon_start=1
/transl_table=11
/product="p28-1"
/protein_id="AA014356.1"
/db_xref="GI:10181084"
/translation="MNNKIKETIINTVLLVCLSLPNISSKAIINNNAKKYGYLISGO
YKRSVSPNSFSYKETIVITKNIILAKDDVDSIETKDSAVGINSBNFTIPTAYVQ
DMSVNEVGTIGYTFAGETRAVEISGSEEFVKNPQGVTTSDARYFPALAREMGNST
PKKRVNSIPIHTWRNDGLSISIVVNCVDFSLNMSISPYICGAGVAIIEFDVL
HIKFAYSKSLGIYSLPSNLSLPASLYHHKMGQFNILNVQVAELASIPKITSAVA
TLNIGYGEIGARLP"
1599..2441
/gene="p28-2"
1599..2441
/gene="p28-2"
/note="outer membrane protein"
/codon_start=1
/transl_table=11
/product="p28-2"
/protein_id="AA014357.1"
/db_xref="GI:10181085"
/translation="MNYKILIVSALISLMSILPYOSFADPVGSRDNDKGFYISAK
YNSISHPKFSAEPIENGTNSLTRKVPGLKKQGDITKKDDTRVAVGIDPNMLIS
LKGDSICYSMDGRILEEAAVQOPNRPNTDNDTNGEYIKHRLSKDMEDQYV
LKDGTTFMSLNTCTIDTRAGVSFPPIACAGIADLTTFYDLNKPAYQGIIGIS
VPTPEVSARIGYHGVIGNKKEKIPVITPVVLPADAPOTTASVTLIDVGFGEIGM
RFPF"
2769..3599
/gene="p28-3"
2769..3599
/gene="p28-3"
/note="outer membrane protein"
/codon_start=1
/transl_table=11
/product="p28-3"
/protein_id="AA014358.1"
/db_xref="GI:10181086"
/translation="MNCCKILITTTIVSLTILPGISFSKPIHNNNTGNPIYIGKV
PSISHGNGFSAKEKNTTGIPLKESWTGIIIDKEHAFFNPISFKENNPLGF
AGVIGYSIPRIEPEVSEYETFPVONPGDFFNDARHYCAISNDSSKMSGKFPVX
NELSDISLMLNVCYDILINKMPSPSYICAGIGTDLIEMPDALNHRAAYQKGRNP
ISBEANISMGVHHKVTNNFRVPLITAGLAPDNLPAIVKLSICFGLFGRVRSF
"
3810..4673
/gene="p28-4"
3810..4673
/gene="p28-4"
/note="outer membrane protein"
/codon_start=1
/transl_table=11
/product="p28-4"
/protein_id="AA014359.1"
/db_xref="GI:10181087"
/translation="MKYKITTYYTALVLTFTTHPIPTSPAPASITIHNFYISGKMP
TASHGIFSAKEQSFYKVLVGLDRLSHNINNDNTASLKVONSPFYKONPLIGF
AGAIGYISNRSIELEVSHEIPDTRKPGNNYINDSHKYLASHGHSICDGNAGVYT
AKTDKSVLLKNELGLDVSFMLNACVDITTEKMPFSYICAGIGTDLISPEETONIS
YQGLGNTYTINGRSVFPAGHGHKVIQNEPKGIPTLLPDGSIKXQGSATVTLVCH
FGLSIGSRFPF"
4970..5821
/gene="p28-5"
4970..5821
/gene="p28-5"
/note="outer membrane protein"
/codon_start=1
/transl_table=11
/product="p28-5"